

Genome Browser

Genome Browser under **Fine Genomes** is a way for selecting and browsing genomes in IMG.

Figure 1(i) shows the tree view of genomes in IMG. Please note that to include Viruses and GFragment (i.e., genome fragments), users will have to change the **Preferences** under **MyIMG**. The initial tree display only shows the domain level. Users can click on the "triangle" to expand to the phylum level as shown in Figure 1(ii). The process can be continued to class, order, etc. Users can also use "Open All" and "Close All" features to expand or close the tree expansion.

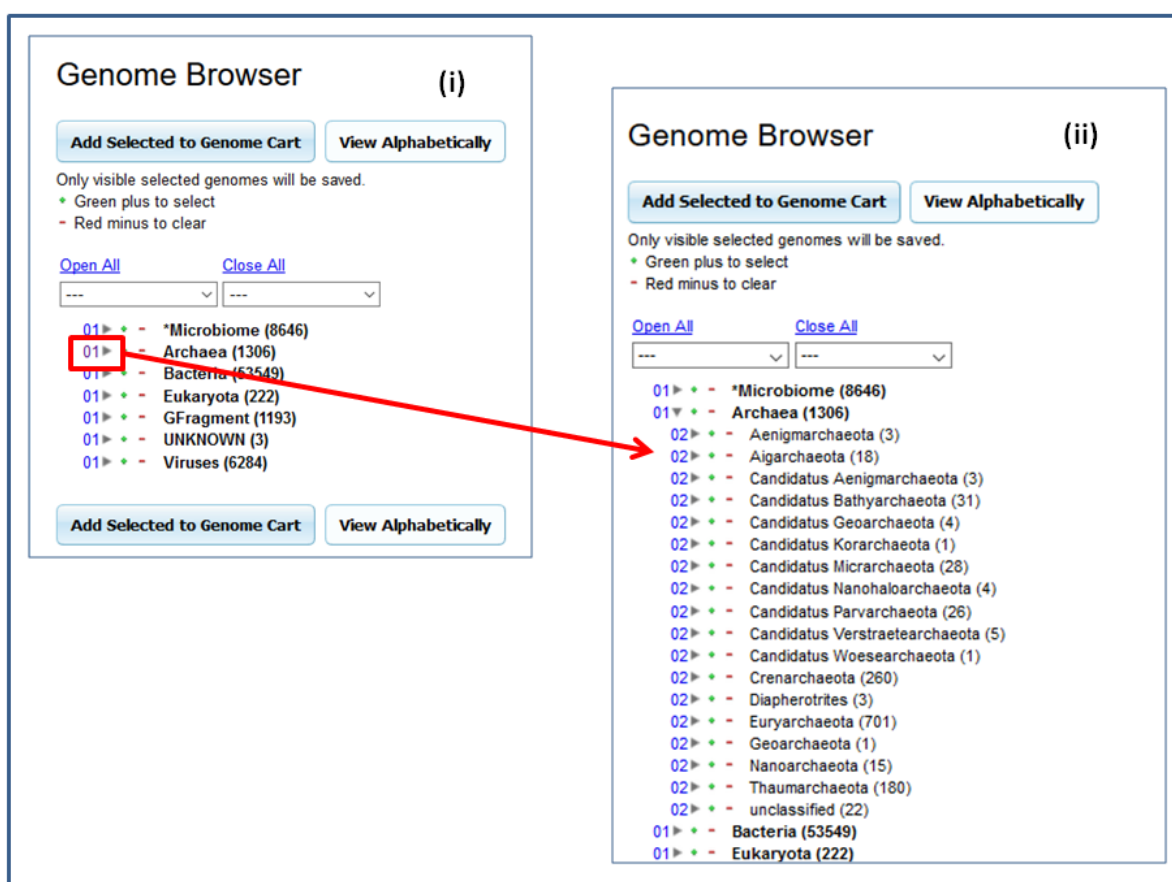


Figure 1. Genome Browser: Tree Display

To view genome list in a table format, simply click the **View Alphabetically** button (in Figure 1(i)). Figure 2 shows the table display of all genomes in IMG.

Genome Browser

[Table Configuration](#)

hint:

Data Statistics with * [assembled, unassembled, both] means metagenomes counts or percentages only use assembled data or unassembled data or both (assembled data and unassembled data) for its calculations. This does not apply to isolates. The [assembled, unassembled, both] pick list is available under the Table Configuration Data Statistics. **The default is assembled data.**

Add Selected to Genome Cart

Select All

Clear All

Filter column: Domain Filter text Apply

Export Page 1 of 713 << first < prev 1 2 3 4 5 6 7 8 9 10 next > last >> 100

Column Selector

Select Page

Deselect Page

Select	Domain	Status	Study Name	Genome Name / Sample Name	Sequencing Center	IMG Genome ID	Genome Size * assembled	Gene Count * assembled
<input type="checkbox"/>	Archaea	Draft	Metagenomics study of hot springs in Tengchong, Yunnan	Unclassified Bathyarchaeota JZ bin 7 (updated)	Beijing Novogene Bioinformatics Technology Co., Ltd	2728369726	1245928	10
<input type="checkbox"/>	Archaea	Finished	Methanothermobacter thermautotrophicus Delta H	Methanothermobacter thermautotrophicus Delta H	Genome Therapeutics	638154510	1751377	10
<input type="checkbox"/>	Archaea	Draft	Hot spring microbial communities from Yellowstone National Park, US	Sulfolobales-MK5-r02	DOE Joint Genome Institute (JGI)	2522572137	1616080	10
<input type="checkbox"/>	Archaea	Permanent Draft	Pan-genome of Methanobrevibacter smithii, in twins	Methanobrevibacter smithii TS146C	Washington University in St. Louis	2547132056	1947483	10

Figure 2. Genome Browser: Table Display

The **Genome Browser** allows user to select or de-select genomes individually or collectively. User can click on the name of an individual genome to view the associated Organism Details. User can also sort the alphabetical list of genomes by clicking on a column name. Alphabetical columns are sorted in ascending alphabetic order. Numeric columns are sorted in ascending numeric order.

User can select genomes with the **Genome Browser** by clicking the checkbox next to each genome, and then clicking on **Add Selected to Genome Cart** button to save the genomes into Genome Cart. User also has the option to “Select All” of the genomes or “Clear All” of the selections.

Table Configuration

By default, the alphabetical list of genomes includes information on domain, sequencing status, study name, genome name, sequencing center, IMG Genome ID, genome size and gene count. However, user can configure the displayed columns by using the **Table Configuration** selector at the bottom of the **Gene Browser** page, as shown in Figure 3.

Table Configuration

Redisplay

☒ Genome Field ☒ Metadata (Updated Jun 19 2017) ☒ Data Statistics

All	Clear	All	Clear	All	Clear	Select Counts	Select Percentage	* Assembled (Metagenomes) v
<input checked="" type="checkbox"/> Domain		<input type="checkbox"/> Alt. Contact Email		<input checked="" type="checkbox"/> * Genome Size (Number of total bases)				
<input checked="" type="checkbox"/> Status		<input type="checkbox"/> Alt. Contact Name		<input checked="" type="checkbox"/> * Gene Count (Number of total Genes)				
<input checked="" type="checkbox"/> Study Name		<input type="checkbox"/> Alt2. Contact Emails (GOLD)		<input type="checkbox"/> * Scaffold Count (Number of scaffolds)				
<input checked="" type="checkbox"/> Genome Name / Sample Name		<input type="checkbox"/> Alt2. Contact Names (GOLD)		<input type="checkbox"/> * CRISPR Count (Number of CRISPRs)				
<input checked="" type="checkbox"/> Sequencing Center		<input type="checkbox"/> Altitude		<input type="checkbox"/> * GC Count (Number of GC)				
<input checked="" type="checkbox"/> IMG Genome ID (IMG Taxon ID)		<input type="checkbox"/> Bioproject Accession		<input type="checkbox"/> * GC (GC % in fraction)				
<input type="checkbox"/> Phylum		<input type="checkbox"/> Biosample Accession		<input type="checkbox"/> Coding Base Count (Total number of coding bases)				
<input type="checkbox"/> Class		<input type="checkbox"/> Biotic Relationships		<input type="checkbox"/> Coding Base Count % (Percentage of Total number of coding bases)				
<input type="checkbox"/> Order		<input type="checkbox"/> Cell Arrangement		<input type="checkbox"/> Coding Base Count NP (Total number of coding bases no pseudogenes)				
<input type="checkbox"/> Family		<input type="checkbox"/> Cell Shape		<input type="checkbox"/> Coding Base Count NP % (Percentage of Total number of coding bases no pseudogenes)				
<input type="checkbox"/> Genus		<input type="checkbox"/> Chlorophyll concentration		<input type="checkbox"/> * CDS Count (Number of CDS genes)				
<input type="checkbox"/> Species		<input type="checkbox"/> Clade		<input type="checkbox"/> * CDS % (Percentage of CDS genes)				
<input type="checkbox"/> IMG Product Assignment		<input type="checkbox"/> Contact Email		<input type="checkbox"/> * RNA Count (Number of RNA genes)				
<input type="checkbox"/> IMG Release		<input type="checkbox"/> Contact Name		<input type="checkbox"/> * RNA %				
<input type="checkbox"/> IMG Submission ID		<input type="checkbox"/> Culture Type		<input type="checkbox"/> * rRNA Count (Number of rRNA genes)				
<input type="checkbox"/> JGI Project ID / ITS PID		<input type="checkbox"/> Cultured		<input type="checkbox"/> * 5S rRNA Count (Number of 5S rRNAs)				
<input type="checkbox"/> JGI Analysis Product Name		<input type="checkbox"/> Depth		<input type="checkbox"/> * 16S rRNA Count (Number of 16S rRNAs)				
<input type="checkbox"/> JGI Analysis Project Type		<input type="checkbox"/> Diseases		<input type="checkbox"/> * 18S rRNA Count (Number of 18S rRNAs)				
<input type="checkbox"/> GOLD Analysis Project ID		<input type="checkbox"/> Ecosystem		<input type="checkbox"/> * 23S rRNA Count (Number of 23S rRNAs)				
<input type="checkbox"/> GOLD Analysis Project Type		<input type="checkbox"/> Ecosystem Category		<input type="checkbox"/> * 28S rRNA Count (Number of 28S rRNAs)				
<input type="checkbox"/> GOLD Sequencing Project ID		<input type="checkbox"/> Ecosystem Subtype		<input type="checkbox"/> * tRNA Count (Number of tRNA genes)				
<input type="checkbox"/> GOLD Study ID		<input type="checkbox"/> Ecosystem Type		<input type="checkbox"/> * Other RNA Count (Number of other unclassified RNA genes)				
<input type="checkbox"/> Add Date		<input type="checkbox"/> Ecotype		<input type="checkbox"/> Pseudo Genes Count (Number of pseudo genes)				
<input type="checkbox"/> Assembly Method		<input type="checkbox"/> Energy Source		<input type="checkbox"/> Pseudo Genes % (Percentage of pseudo genes)				

Figure 3. Table Configuration.

There are 3 categories of genome information:

1. *Genome Field*: Information regarding a genome such as phylogeny (phylum, class, ...), associated JGI and GOLD IDs, assembly method, etc.
2. *Metadata*: Genome associated metadata imported from GOLD (updated daily) such as altitude, latitude, culture type, ecosystem information, etc.
3. *Data Statistics*: Genome statistics information such as scaffold count, base count, gene count, etc. For metagenomes, there is an additional option to show assembled data, unassmebled data or both. (See the red rectangle near the upper right corner in Figure 3.)

Users will have to click the **Redisplay** button after any changes to the table configuration selection in order to view the changes.